



# 9

4-31193A.ST25.txt  
SEQUENCE LISTING

&lt;110&gt; Novartis AG

&lt;120&gt; Selectable Marker Genes

&lt;130&gt; 4-31193A

&lt;160&gt; 10

&lt;170&gt; PatentIn version 3.0

&lt;210&gt; 1

&lt;211&gt; 2607

&lt;212&gt; DNA

&lt;213&gt; homo sapiens

&lt;400&gt; 1

atgagagagc tcgtcaacat tccactggta catattctta ctctggttgc cttcagcgga  
60actgagaaac ttccaaaagc tccgtgtcatc accactcctc ttgaaacagt ggatgcctta 1  
20gttgaagaag tggctacttt catgtgtgca gtggaatcct acccccagcc tgagatttcc 1  
80tggactagaa ataaaattct cattaaactc tttgacaccc ggtacagcat ccgggagaat 2  
40gggcagctcc tcaccatcct gagtgtggaa gacagtgatg atggcattta ctgctgcacg 3  
00gccaacaatg gtgtgggagg agctgtggag agttgtggag ccctgcaagt gaagatgaaa 3  
60cctaaaataa ctgctcctcc cataaatgtg aaaataatag agggattaaa agcagtccta 4  
20ccatgtacta caatgggtaa tcccaaacca tcagtgtctt ggataaaggg agacagccct 4  
80ctcagggaaa attcccgaat tgcagttctt gaatctggga gcttgaggat tcataacgta 5  
40caaaaggaag atgcaggaca gtatcgatgt gtggcaaaaa acagcctcgg gacagcatat 6  
00

4-31193A.ST25.txt

B1  
 C1  
 tccaaagtgg tgaagctgga atttgagggtt ttgcccagga tcctgcgggc tcctgaatcc 6  
 60  
 cacaatgtca cctttggctc ctttgtgacc ctgcactgta cagcaacagg cattcctgtc 7  
 20  
 cccaccatca cctggattga aaacggaaat gctgtttctt ctgggtccat tcaagagagt 7  
 80  
 gtgaaagacc gagtgattga ctcaagactg cagctgttta tcaccaagcc aggactctac 8  
 40  
 acatgcatag ctaccaataa gcatggggag aagttcagta ctgccaaggc tgcagccacc 9  
 00  
 atcagcatag cagaatggag taaaccacag aaagataaca aaggctactg cgcccagtac 9  
 60  
 agaggggagg tgtgtaatgc agtcctggca aaagatgctc ttgtttttct caacacctcc 10  
 20  
 tatgcccacc ctgaggaggc ccaagagcta ctggtccaca cggcctggaa tgaactgaaa 10  
 80  
 gtagtgagcc cagtctgccg gccagctgct gaggctttgt tgtgtaacca catcttccag 11  
 40  
 gagtgcagtc ctggagtagt gcctactcct attcccattt gcagagagta ctgcttggca 12  
 00  
 gtaaaggagc tcttctgcgc aaaagaatgg ctggtaatgg aagagaagac ccacagagga 12  
 60  
 ctctacagat ccgagatgca ttgtctgtcc gtgccaaaat gcagcaagct tcccagcatg 13  
 20  
 cattgggacc ccacggcctg tgccagactg ccacatctag attataacaa agaaaaccta 13  
 80  
 aaaacattcc caccaatgac gtcctcaaag ccaagtgtgg acattccaaa tctgccttcc 14  
 40  
 tcctcctctt cttccttctc tgtctcacct acatactcca tgactgtaat aatctccatc 15  
 00  
 atgtccagct ttgcaatatt tgtgcttctt accataacta ctctctattg ctgccgaaga 15  
 60

B1  
C1

4-31193A.ST25.txt

agaaaacaat ggaaaaataa gaaaagagaa tcagcagcag taaccctcac cacactgcct 16  
20

tctgagctct tactagatag acttcatccc aaccccatgt accagaggat gccgctcctt 16  
80

ctgaacccca aattgctcag cctggagtat ccaaggaata acattgaata tgtgagagac 17  
40

atcggagagg gagcgtttgg aagggtgttt caagcaaggg caccaggctt acttccttat 18  
00

gaacctttca ctatggtggc agtaaagatg ctcaaagaag aagcctcggc agatatgcaa 18  
60

gcggactttc agagggaggc agcctcatg gcagaatttg acaaccctaa cattgtgaag 19  
20

ctattaggag tgtgtgctgt cgggaagcca atgtgcctgc tctttgaata catggcctat 19  
80

ggtgacctca atgagttcct ccgcagcatg tcccctcaca ccgtgtgcag cctcagtcac 20  
40

agtgacttgt ctatgagggc tcaggtctcc agccctgggc cccaccacct ctccctgtgct 21  
00

gagcagcttt gcattgccag gcaggtggca gctggcatgg cttacctctc agaacgtaag 21  
60

tttgttcacc gagatttagc caccaggaac tgccctgggtgg gcgagaacat ggtggtgaaa 22  
20

attgccgact ttggcctctc caggaacatc tactcagcag actactacaa agctaatagaa 22  
80

aacgacgcta tccctatccg ttggatgcca ccagagtcga ttttttataa ccgctacact 23  
40

acagagtctg atgtgtgggc ctatggcgtg gtccctctggg agatcttctc ctatggcctg 24  
00

cagccctact atgggatggc ccatgaggag gtcatttact acgtgcgaga tggcaacatc 24  
60

ctctcctgcc ctgagaactg ccccgaggag ctgtacaatc tcatgcgtct atgttgagac 25  
20

31  
C1

4-31193A.ST25.txt

aagctgcctg cagacagacc cagtttcacc agtattcacc gaattctgga acgcatgtgt 25  
80

gagagggcag aggggaactgt gagtgtc 26  
07

<210> 2  
<211> 869  
<212> PRT  
<213> homo sapiens

<400> 2

Met Arg Glu Leu Val Asn Ile Pro Leu Val His Ile Leu Thr Leu Val  
1 5 10 15

Ala Phe Ser Gly Thr Glu Lys Leu Pro Lys Ala Pro Val Ile Thr Thr  
20 25 30

Pro Leu Glu Thr Val Asp Ala Leu Val Glu Glu Val Ala Thr Phe Met  
35 40 45

Cys Ala Val Glu Ser Tyr Pro Gln Pro Glu Ile Ser Trp Thr Arg Asn  
50 55 60

Lys Ile Leu Ile Lys Leu Phe Asp Thr Arg Tyr Ser Ile Arg Glu Asn  
65 70 75 80

Gly Gln Leu Leu Thr Ile Leu Ser Val Glu Asp Ser Asp Asp Gly Ile  
85 90 95

Tyr Cys Cys Thr Ala Asn Asn Gly Val Gly Gly Ala Val Glu Ser Cys  
100 105 110

Gly Ala Leu Gln Val Lys Met Lys Pro Lys Ile Thr Arg Pro Pro Ile  
115 120 125

Asn Val Lys Ile Ile Glu Gly Leu Lys Ala Val Leu Pro Cys Thr Thr  
130 135 140

Met Gly Asn Pro Lys Pro Ser Val Ser Trp Ile Lys Gly Asp Ser Pro  
145 150 155 160

Leu Arg Glu Asn Ser Arg Ile Ala Val Leu Glu Ser Gly Ser Leu Arg  
165 170 175

Ile His Asn Val Gln Lys Glu Asp Ala Gly Gln Tyr Arg Cys Val Ala

180

185

190

Lys Asn Ser Leu Gly Thr Ala Tyr Ser Lys Val Val Lys Leu Glu Phe  
 195 200 205

Glu Val Phe Ala Arg Ile Leu Arg Ala Pro Glu Ser His Asn Val Thr  
 210 215 220

Phe Gly Ser Phe Val Thr Leu His Cys Thr Ala Thr Gly Ile Pro Val  
 225 230 235 240

Pro Thr Ile Thr Trp Ile Glu Asn Gly Asn Ala Val Ser Ser Gly Ser  
 245 250 255

Ile Gln Glu Ser Val Lys Asp Arg Val Ile Asp Ser Arg Leu Gln Leu  
 260 265 270

Phe Ile Thr Lys Pro Gly Leu Tyr Thr Cys Ile Ala Thr Asn Lys His  
 275 280 285

Gly Glu Lys Phe Ser Thr Ala Lys Ala Ala Ala Thr Ile Ser Ile Ala  
 290 295 300

Glu Trp Ser Lys Pro Gln Lys Asp Asn Lys Gly Tyr Cys Ala Gln Tyr  
 305 310 315 320

Arg Gly Glu Val Cys Asn Ala Val Leu Ala Lys Asp Ala Leu Val Phe  
 325 330 335

Leu Asn Thr Ser Tyr Ala Asp Pro Glu Glu Ala Gln Glu Leu Leu Val  
 340 345 350

His Thr Ala Trp Asn Glu Leu Lys Val Val Ser Pro Val Cys Arg Pro  
 355 360 365

Ala Ala Glu Ala Leu Leu Cys Asn His Ile Phe Gln Glu Cys Ser Pro  
 370 375 380

Gly Val Val Pro Thr Pro Ile Pro Ile Cys Arg Glu Tyr Cys Leu Ala  
 385 390 395 400

Val Lys Glu Leu Phe Cys Ala Lys Glu Trp Leu Val Met Glu Glu Lys  
 405 410 415

Thr His Arg Gly Leu Tyr Arg Ser Glu Met His Leu Leu Ser Val Pro  
 420 425 430

Lys Cys Ser Lys Leu Pro Ser Met His Trp Asp Pro Thr Ala Cys Ala

435

440

445

Arg Leu Pro His Leu Asp Tyr Asn Lys Glu Asn Leu Lys Thr Phe Pro  
 450 455 460

Pro Met Thr Ser Ser Lys Pro Ser Val Asp Ile Pro Asn Leu Pro Ser  
 465 470 475 480

Ser Ser Ser Ser Ser Phe Ser Val Ser Pro Thr Tyr Ser Met Thr Val  
 485 490 495

Ile Ile Ser Ile Met Ser Ser Phe Ala Ile Phe Val Leu Leu Thr Ile  
 500 505 510

Thr Thr Leu Tyr Cys Cys Arg Arg Arg Lys Gln Trp Lys Asn Lys Lys  
 515 520 525

Arg Glu Ser Ala Ala Val Thr Leu Thr Thr Leu Pro Ser Glu Leu Leu  
 530 535 540

Leu Asp Arg Leu His Pro Asn Pro Met Tyr Gln Arg Met Pro Leu Leu  
 545 550 555 560

Leu Asn Pro Lys Leu Leu Ser Leu Glu Tyr Pro Arg Asn Asn Ile Glu  
 565 570 575

Tyr Val Arg Asp Ile Gly Glu Gly Ala Phe Gly Arg Val Phe Gln Ala  
 580 585 590

Arg Ala Pro Gly Leu Leu Pro Tyr Glu Pro Phe Thr Met Val Ala Val  
 595 600 605

Lys Met Leu Lys Glu Glu Ala Ser Ala Asp Met Gln Ala Asp Phe Gln  
 610 615 620

Arg Glu Ala Ala Leu Met Ala Glu Phe Asp Asn Pro Asn Ile Val Lys  
 625 630 635 640

Leu Leu Gly Val Cys Ala Val Gly Lys Pro Met Cys Leu Leu Phe Glu  
 645 650 655

Tyr Met Ala Tyr Gly Asp Leu Asn Glu Phe Leu Arg Ser Met Ser Pro  
 660 665 670

His Thr Val Cys Ser Leu Ser His Ser Asp Leu Ser Met Arg Ala Gln  
 675 680 685

Val Ser Ser Pro Gly Pro Pro Pro Leu Ser Cys Ala Glu Gln Leu Cys

690

695

700

Ile Ala Arg Gln Val Ala Ala Gly Met Ala Tyr Leu Ser Glu Arg Lys  
705 710 715 720

Phe Val His Arg Asp Leu Ala Thr Arg Asn Cys Leu Val Gly Glu Asn  
725 730 735

Met Val Val Lys Ile Ala Asp Phe Gly Leu Ser Arg Asn Ile Tyr Ser  
740 745 750

Ala Asp Tyr Tyr Lys Ala Asn Glu Asn Asp Ala Ile Pro Ile Arg Trp  
755 760 765

Met Pro Pro Glu Ser Ile Phe Tyr Asn Arg Tyr Thr Thr Glu Ser Asp  
770 775 780

Val Trp Ala Tyr Gly Val Val Leu Trp Glu Ile Phe Ser Tyr Gly Leu  
785 790 795 800

Gln Pro Tyr Tyr Gly Met Ala His Glu Glu Val Ile Tyr Tyr Val Arg  
805 810 815

Asp Gly Asn Ile Leu Ser Cys Pro Glu Asn Cys Pro Val Glu Leu Tyr  
820 825 830

Asn Leu Met Arg Leu Cys Trp Ser Lys Leu Pro Ala Asp Arg Pro Ser  
835 840 845

Phe Thr Ser Ile His Arg Ile Leu Glu Arg Met Cys Glu Arg Ala Glu  
850 855 860

Gly Thr Val Ser Val  
865

<210> 3

<211> 25

<212> DNA

<213> homo sapiens

<400> 3

cgtcctgcgt gagcctggat taatc  
25

<210> 4

<211> 25

<212> DNA

<213> homo sapiens

<400> 4

gcctggatta atcatgagag agctc  
25

<210> 5

<211> 42

<212> DNA

<213> homo sapiens

<400> 5

cgaggcctgt cttcaacctt agacactcac agttccctct gc  
42

<210> 6

<211> 27

<212> DNA

<213> homo sapiens

<400> 6

cggcctgtgc cagactgcca catctag  
27

<210> 7

<211> 32

<212> DNA

<213> homo sapiens

<400> 7

cgtctaggtg agggttactg ctgctgattc tc  
32

<210> 8

<211> 38

<212> DNA

<213> homo sapiens

<400> 8

ggttaaccct attcaatgtt attccttgaa tactccag  
38

<210> 9



B1  
Dut CT

4-31193A.ST25.txt

<211> 24  
<212> DNA  
<213> homo sapiens

<400> 9  
cttccaaaag ctctgtcat cacc  
24

<210> 10  
<211> 26  
<212> DNA  
<213> homo sapiens

<400> 10  
ccagtcattgg agtatgtagg tgagac  
26